Spring 2005

BIO/CS 271: Introduction to Bioinformatics

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BIO/CS 271 – Introduction to Bioinformatics

Spring Quarter, 2005

2:15-3:30 T TH, 105 BH

BIO/CS 271 Introduction to Bioinformatics: Introduction to DNA as an information storage system, data searches and pairwise alignments, substitution patterns, protein folding, and proteomics. Prerequisite: CS 240 or equivalent, BIO 112

Faculty

Dr. Dan Krane: 126 BH (775-2257), dan.krane@wright.edu.
Office hours: 1:00-1:45 T TH, or by appointment
Dr. Travis Doom 331 RC (775-5105), travis.doom@wright.edu.
Office hours: 3:45-5:00 T TH, or by appointment

Course Materials

Required Textbook: D. Krane and M. Raymer, **Fundamental Concepts of Bioinformatics**, Benjamin Cummings, 2003.
Course Website: http://birg.cs.wright.edu/cs271

Grading Policies

Grades will be based on the two regular period exams (100 pts. each), a final cumulative exam (150 pts.) and the completion of lab and homework assignments made in class (50 pts.). One cumulative make-up exam will be given after the normal class meeting time on Tuesday, May 31. Only those students who present a valid reason for missing the original exam at least *two days before* the exam date or documentation of a medical emergency will be eligible to take the make-up exam.

Grades will be determined via standard cutoffs (100-90% A, 89-80% B, 79-70% C, 69-60% D, <60% F). The instructors reserve the right to lower minimum requirements ("curve") for final grades based upon the final point distribution; grade requirements will not be increased.

Homework assignments (labs) are due at specified times. Late programming assignments will be accepted, but 10% of the total available points will be deducted for each day late. Labs are considered one day late each 24 hour period after the original due date. A homework assignment will not be accepted late after it has been graded and returned to other students.

Collaboration: Discussion of course contents with other students is an important part of the academic process and is encouraged. However, it is expected that course programming assignments, homeworks, and other course assignments will be completed *on an individual basis* unless the assignment specifically states otherwise.

Students may discuss general concepts with one another, but may not, under any circumstances, work together on the actual implementation of any course assignment. *If you work with other students on "general concepts" be certain to acknowledge the collaboration and its extent in the assignment. Unacknowledged collaboration will be considered dishonest.* "Code sharing" (including code from previous quarters) is strictly disallowed. "Copying" or significant collaboration on any graded assignments will be considered a violation of the university guidelines for academic honesty.

If the same work is turned in by two or more students, all parties involved will be held equally accountable for violation of academic integrity. *You are responsible for ensuring that other students do not have access to your work*: do not give another student access to your account, do not leave printouts in the recycling bin, pick up your printouts promptly, do not leave your workstation unattended, etc. If you suspect that your work has been compromised notify an instructor immediately.

Note: Failure to attend the first day of class, during which time these academic honesty policies will be explained in detail, *does not excuse you from following these policies*. If you have any questions about collaboration or any other issues related to academic integrity, please see an instructor immediately for clarification.

(OVER)

COURSE CONTENT & TENTATIVE LECTURE SCHEDULE

PART I. DNA'S INFORMATION CONTENT AND BASIC PERL

Date	Topics
T 3/29	Course Introduction, Information storage in DNA
R 3/31	Introduction to Unix & Perl
T 4/5	Introduction to Genomics: Data searches and pairwise alignments
R 4/7	Basic Perl: array variables and control structures
T 4/12	Tools of molecular biology, molecular data repositories
R 4/14	Perl Programming: Functions and subroutines
T 4/19	Midterm Exam #1 (100 pts.)

PART II. GENOMIC INFORMATION CONTENT

Date	Topics
R 4/21	Intermediate Perl: Arrays and hashes, File I/O
T 4/26	Substitution patterns
R 4/28	Cluster analysis and phylogenetics
T 5/3	Parsimony approaches to phylogenetics
R 5/5	Prokaryotic and eukaryotic genomes & gene structures
T 5/10	Gene recognition
R 5/12	Gene expression and microarrays
T 5/17	Midterm Exam #1 (100 pts.)

PART III. PROTEOMIC INFORMATION CONTENT

Date	Topics
R 5/19	Predicting RNA secondary structure
T 5/24	Phi/psi, protein secondary structure, X-ray structures
R 5/26	Protein folding – simple models
T 5/31	Structural modeling and visualization
R 6/2	Proteomics, protein classification and modification
R 6/9	Final Examination (150 pts.); 3:15-5:15, 105 BH